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Marine Ecology: Reaping the Benefits of Local Dispersal

A central question of marine ecology is, how far do larvae disperse? Evidence is accumulating that the probability of dispersal declines rapidly with distance. This provides an incentive for communities to manage their own fish stocks and cooperate with neighbors.

Peter M. Buston and Cassidy C. D'Aloia

Patterns of larval dispersal and population connectivity are the big black box of marine ecology. Understanding what is going on inside this black box is essential if we are to better understand marine population dynamics and to better manage marine fish populations. The reason is simple: most marine fishes have a two-stage life cycle composed of a relatively sedentary adult stage and a relatively dispersive larval stage. This means that fish live in spatially restricted populations that are connected by larval dispersal to form metapopulations: population dynamics are driven by birth rates and death rates within populations, and by rates of larval exchange between populations [1]. On paper, we know what we need to do — measure patterns of larval dispersal and determine what causes variation across species and seascapes — and this seems straightforward enough. However, this is enormously challenging because larvae spend weeks developing as tiny propagules in the vast open ocean environment [2]. In spite of the challenges involved, some amazing progress has been made over the last 15 years, primarily studying small, tractable coral reef fishes. Most research to date, however, has focused on these model species at small spatial scales. But now, a new study by Almany *et al.* [3] in a recent issue of *Current Biology* makes major progress by quantifying patterns of dispersal in a large, commercially important fish at a scale relevant to local conservation planning.

During the 1980s and 1990s, indirect evidence had been accumulating that reef fish larvae might not always disperse far from their natal population [4–6]. However, in 1999, two papers, published in the same issue of *Nature*, caused a paradigm shift, as they provided direct evidence that a large fraction of larvae recruit to their natal population using otolith chemical tagging and trace element signatures [7,8]. Since then, dispersal research has proliferated — the first decade of the 21st century has even been dubbed the 'decade of connectivity' for coral reef ecology [9]. Much of this progress is attributable to the application of molecular genetic techniques on a large scale. In 2005, Jones *et al.* [10], used genetic parentage analysis to measure dispersal in marine systems for the first time, and showed that within a single population of the panda clownfish *Amphiprion polymnus* one third of recruits returned to their one kilometer square natal area. At this point it was clear that, for at least some reef fish species, a large proportion of offspring settle in or near their natal populations. Since then, some of the major achievements include documenting dispersal among populations within a metapopulation [11], quantifying how the probability of dispersal changes with distance at a small spatial scale [12], and shifting the focus from small, tractable species to large, exploited species [13]. Now, Almany *et al.* [3] take another step forward, collecting enough empirical data to directly test which function best describes the pattern of dispersal in a large, exploited species.

Almany *et al.* [3] used a massive field effort and genetic parentage analysis to measure patterns of larval dispersal of the squaretail coral grouper *Plectropomus areolatus* (Figure 1) up to 33 km from their natal site, off the beautiful island of Manus in Papua New Guinea. Their study area includes five customary marine tenure

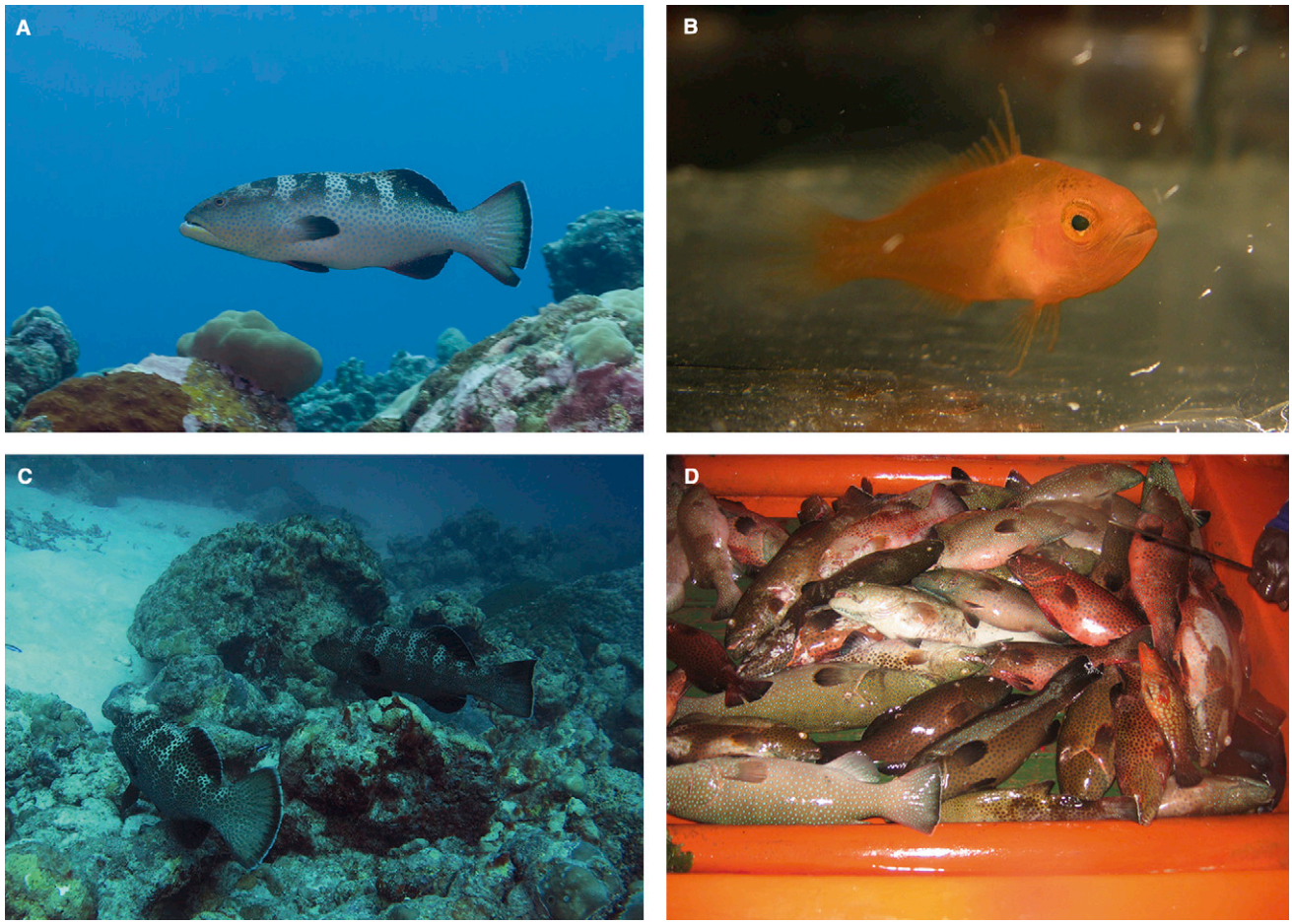

Figure 1. Life cycle of the squaretail coral grouper (*Plectropomus areolatus*).

The squaretail coral grouper is found in shallow coral reef habitats throughout the IndoPacific [16]. Squaretail coral grouper have a bi-partite life cycle composed of a relatively site-restricted reef resident (juvenile and adult) phase [17] (A) and a relatively dispersive larval phase [3] (B; *Plectropomus* sp.). (C) Like many other grouper species, squaretail coral grouper periodically aggregate in large numbers, at certain reef locations, to spawn [18]. (D) This makes them particularly vulnerable to overfishing because fishermen can target and decimate these spawning aggregations [19]. Fishermen and conservationists alike are interested in this species because it is the focus of both local and regional fisheries [20]. (Photos: (A) Steve Lindfield; (B) Colin Wen; (C) Rucha Karkarey: Science and Conservation of Fish Aggregations; (D) Alec Hughes.)

areas (CMTs) — very small, locally-managed areas of coral reef. Over a two-week period, with the help of local fishermen and while camped out on a large canoe, they collected tissue samples from hundreds of adult grouper at a single focal spawning aggregation within one CMT. Spawning aggregations occur when individuals gather periodically at a particular reef location to breed (Figure 1). Months later, they sampled hundreds of juvenile grouper from reefs distributed across five CMTs and 75 km of coastline, and used standard parentage analysis to assign 76 of the sampled juveniles to the sampled adults. They show that the proportion of juveniles assigned to adults was highest for the CMT containing the focal spawning aggregation and lowest for the CMT most distant from the focal spawning aggregation. Further, they evaluated alternative functions for the shape of the relationship between the likelihood of dispersal and distance. This mammoth empirical effort confirms, for a large, exploited, coral reef fish species, what a cadre of marine ecologists have suspected for the last decade or so — that the probability of successful larval dispersal declines rapidly as a function of distance from the natal site.

How do these results influence the way we think about the management of marine fish populations? Many marine ecologists, government and non-governmental organizations would like to see people fishing less, and avoiding sites that are critical for key events in the fish's life history, such as spawning aggregations, so that populations can recover and fishing can become more sustainable [14]. However, getting fishermen to comply with restrictions is challenging, because fish is the primary source of nutrition and income for many communities. The most effective way to get people to fish less is to offer them incentives to do so, especially when the costs of policing are high, as they are in many remote areas. The best incentives will be those that provide direct and near immediate benefits. Almany *et al.* [3] provide clear evidence that by harvesting fewer adult fish, communities are likely to benefit directly from their own actions: nearly 20% of juveniles in one CMT area came from the fish spawning aggregation located within it. They also show that

such actions create benefits for neighboring communities, creating an incentive for pair-wise cooperation between them: approximately 13% of the juveniles in two CMTs came from the fish spawning aggregation in the CMT next door. Indeed, their findings were well-received by the five communities and resulted in the shift from individually-managed tenure areas to a single, cooperatively-managed fishery.

Almany *et al.*'s findings [3] make an important contribution to the study of marine larval dispersal and population connectivity by showing that the probability of successful larval dispersal declines with distance for a large, exploited species just as it does for small, tractable species. This qualitative result seems robust, even if the broad confidence intervals prevent us from making quantitative predictions about the probability of larval exchange between populations. The next big challenge will be to shift from descriptive models of dispersal to models that make precise quantitative predictions. It is only by the development of predictive models that we can begin to understand how population connectivity will (or will not) change under alternative management actions. To accomplish this, we must increase massively the amount of empirical data collected. With sufficient data, we will be able to test which dispersal curve, from a competing set of curves, has the greatest predictive skill, by using withheld data or new data collected at different times or places. The collection of large datasets will also enable us to integrate direct measures of dispersal with other approaches to studying larval dispersal. For example, such datasets will enable us to test the predictive skill of alternative coupled biophysical models, which simulate dispersal via oceanographic flow and larval behavior [15]. This will be an important step toward a more complete understanding of the patterns of dispersal, because such biophysical models, once validated, might be used to predict the patterns of dispersal in species that are not amenable to direct genetic studies.

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